

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 21:52:48 ; Search time 1873 Seconds

(without alignments)
7893.340 Million cell updates/sec

Title: US-09-914-324A-3

Perfect score: 508
Sequence: 1 cccaaaatgagcgagcagat.....aaagtcagttgattcttgg 508

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_da:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
8: gb_ph:*
9: gb_pl:*
10: gb_pl:*
11: gb_pl:*
12: gb_pl:*
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15: gb_pl:*
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38: gb_pl:*
39: gb_pl:*
40: gb_pl:*
41: gb_pl:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	508	100.0	508	9	AF140598	AF140598 Homo sapi
2	495	97.4	544	9	BC001466	BC001466 Homo sapi
3	493.4	97.1	554	9	BC017370	BC017370 Homo sapi
4	471	92.7	497	9	H007060A05	AF085906 Homo sapi
5	415	81.7	3208	6	AX212267	AX212267 Sequence
6	392	77.2	433	11	G27926	G27926 human STS S
7	347.2	68.3	104787	9	AC109638	AC109638 Homo sapi
8	332.2	65.4	1616	10	BC027396	BC027396 Homo sapi
9	332.2	64.4	1616	10	AF142059	AF142059 Homo sapi
10	323	63.6	504	10	AF140599	AF140599 Mus muscu
11	304.6	60.0	173346	9	AC112184	AC112184 Homo sapi
12	304.6	60.0	175561	9	AC012636	AC012636 Homo sapi
13	304.4	59.9	306	9	AY099360	AY099360 Homo sapi
14	301.2	59.3	5347	6	AX281690	AX281690 Sequence
15	296.8	58.4	3484	9	HSMEST	X73608 H. sapiens m
16	272.8	53.7	418	6	AX332170	AX332170 Sequence
17	263.6	51.9	1871	9	AK090764	AK090764 Homo sapi
18	239.2	47.1	1933	5	AY027936	AY027936 Salmo sal
19	229.4	45.2	171237	2	AC123343	AC123343 Rattus no
20	198.2	39.0	1181	3	AY119265	AY119265 Drosophila
21	191	37.6	202	6	AX261815	AX261815 Sequence
22	176.4	34.7	46381	9	HSAS54C12	AL080242 Human DNA
23	176.2	34.7	361	3	AB077287	AB077287 Caenorhab
24	175.6	34.6	177444	2	AC024617	AC024617 Homo sapi
25	174.2	34.3	544	8	AY114719	AY114719 Arabidops
26	174.2	34.3	635	8	AY086913	AY086913 Arabidops
27	174.2	34.3	666	8	AY072430	AY072430 Arabidops
28	173	34.1	357	8	AY052401	AY052401 Arabidops
29	162	31.9	324	8	AF179228	AF179228 Schistosac
30	152.2	30.0	46630	2	AC020129	AC020129 Drosophila
31	152.2	30.0	161668	3	AC104602	AC104602 Drosophila
32	152.2	30.0	299970	3	AE003418	AE003418 Drosophila
33	152.2	30.0	299970	3	AE003418	AE003418 Drosophila
34	138.2	27.2	553	3	AY070810	AY070810 Drosophila
35	138.2	27.2	750	3	AF218290	AF218290 Drosophila
36	138.2	27.2	3185	3	AY061302	AY061302 Drosophila
37	138.2	27.2	95294	2	AC019742	AC019742 Drosophila
38	138.2	27.2	167977	3	AC010010	AC010010 Drosophila
39	138.2	27.2	310120	3	AE003468	AE003468 Drosophila
40	133.8	26.3	39874	3	CEZK287	Z70757 Caenorhabdi
41	128	25.2	40197	3	CBR633P21	AC084553 Caenorhab
42	126.2	24.8	1255	8	SCYOL134C	Z74876 S.cerevisia
43	126.2	24.8	12805	8	SCYOL134C	X95465 S.cerevisia
44	98	19.3	164399	3	PFMAL3P6	Z98551 Plasmodium
45	96.6	19.0	146163	2	AC111860	AC111860 Rattus no

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
AF140598	AF140598	Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.	AF140598	GI:4769003		Homo sapiens.		1 (bases 1 to 508)	Kamura,T., Koepf,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J., Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Ellledge,S.J., Conaway,R.C., Harper,J.W. and Conaway,J.W.
AF140598	AF140598	508 bp mRNA							
AF140598	AF140598	linear							
AF140598	AF140598	PRI 11-MAY-1999							

Prod. No. is the number of results predicted by chance to have a

TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase
JOURNAL Science 284 (5414), 657-661 (1999)
MEDLINE 99234320
PUBMED 10213691
REFERENCE 2 (bases 1 to 508)
AUTHORS Kanure, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA

FEATURES
SOURCE
1. 508
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 508
/gene="RBX1"
7. 333
/gene="RBX1"
/note="ring finger-like protein; component of VHL tumor suppressor complex and SCF ubiquitin ligase"
/product="ring-box protein 1"
/protein_id="AAD29715.1"
/db_xref="GI:4769004"
/translation="MAAMDVDPGSGNSGAGKKRFEVKKMNAVALMAMDIYDNCALCRNIMDLICECANQASATSECTVAMGVGNHAFHCHISRLKTRQVPLDREMEFOKYGH"

BASE COUNT 126 a 106 c 124 g 152 t
ORIGIN

Query Match 100.0%; Score 508; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.1e-126;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CCCAAATGGCGGCGAGCATGTGATACCCGAGCGGACACAGCGCGCGGCG 60
Db 1 CCCAAATGGCGGCGAGCATGTGATACCCGAGCGGACACAGCGCGCGGCG 60
OY 61 AAGAGCGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 120
Db 61 AAGAGCGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 120
OY 121 GTTATACCTGTCATCTGCAAGAACCATATATGATCTTTGATAGATGTCA 180
Db 121 GTTATACCTGTCATCTGCAAGAACCATATATGATCTTTGATAGATGTCA 180
OY 181 AACGAGCGCTCCGCTACTTCAAGAGAGTACTGTGCGATGGGAGTCTGA 240
Db 181 AACGAGCGCTCCGCTACTTCAAGAGAGTACTGTGCGATGGGAGTCTGA 240
OY 241 TTTCACCTGCACATCTCTCGCTGAGTCAAAACAGACAGAGTGTCTCA 300
Db 241 TTTCACCTGCACATCTCTCGCTGAGTCAAAACAGACAGAGTGTCTCA 300
OY 301 AGAGAGTGGGAATTCACAAATATAGGAGTGAAGAAAGTCTTCCATCA 360
Db 301 AGAGAGTGGGAATTCACAAATATAGGAGTGAAGAAAGTCTTCCATCA 360
OY 361 TGTATTGTTATTCATTTAATGACTTCCCTGCTGTCTACTAATTAACA 420
Db 361 TGTATTGTTATTCATTTAATGACTTCCCTGCTGTCTACTAATTAACA 420
OY 421 CTGCTGTTTTTCTGCTTTGTTTTTTCAGTTGCTGTTCTGTAAGCCAT 480
Db 421 CTGCTGTTTTTCTGCTTTGTTTTTTCAGTTGCTGTTCTGTAAGCCAT 480
OY 481 TGTCAATAAAGTCCAGTTGATCTCG 508
Db 481 TGTCAATAAAGTCCAGTTGATCTCG 508

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RESULT 2
BC001466

LOCUS BC001466 544 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, ring-box 1, clone MGC:1481 IMAGE:3138751, mRNA,
complete cds.
ACCESSION BC001466
VERSION BC001466.1 GI:12655214
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT
NHL-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boufard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastaglio, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurugan, C., Vogt, J.L., Walker, M.A., Zhang, L. H. and Green, E.D.

FEATURES
source
1. 544
/organism="Homo sapiens"
/db_xref="LocusID:9978"
/db_xref="taxon:9606"
/clone="MGC:1481 IMAGE:3138751"
/tissue_type="Placenta, choriocarcinoma"
/clone_id="NH_MGC_21"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
15. 341
/codon_start=1
/product="ring-box 1"
/protein_id="AAH01466.1"
/db_xref="GI:12655215"
/translation="MAAMDVDPGSGNSGAGKKRFEVKKMNAVALMAMDIYDNCALCRNIMDLICECANQASATSECTVAMGVGNHAFHCHISRLKTRQVPLDREMEFOKYGH"

BASE COUNT 157 a 107 c 129 g 151 t
ORIGIN

Query Match 97.4%; Score 495; DB 9; Length 544;
Best Local Similarity 99.8%; Pred. No. 1.9e-122;
Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 2 CCAAAATGGCGGCGAGCATGTGATACCCGAGCGGACACAGCGCGGCGCA 61
Db 10 CCAAAATGGCGGCGAGCATGTGATACCCGAGCGGACACAGCGCGGCGCA 69
OY 62 AGAAGCGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
Db 70 AGAAGCGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 129
OY 122 TTGATACCTGTCATCTGCAAGAACCATATATGATCTTTGATAGATGTCA 181

```


JOURNAL Unpublished
REFERENCE 2 (bases 1 to 497)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
SUBMITTED BY: Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@wustl.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

SIMILARITY INFORMATION:
similar to Caenorhabditis elegans protein Z70757 (PID:g1262999)
ZK287.5

The location of this clone is unknown.

FEATURES
source
Location/Qualifiers

1..497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:200144"
/clone_lib="Sources:fetal_liver_spleen_1NPLS"
3..305
/note="similar to Caenorhabditis elegans protein Z70757 (PID:g1262999)"
18..284
/note="similar to Caenorhabditis elegans protein U80449 (PID:g1707068)"
36..302
/note="similar to Saccharomyces cerevisiae protein S66830 (PID:g2132017)"
42..302
/note="similar to Schizosaccharomyces pombe protein Z98977 (PID:g2388937)"
51..284
/note="similar to Caenorhabditis elegans protein Z46242 (PID:g559430)"
misc_feature
misc_feature
misc_feature
misc_feature

BASE COUNT 131 a 101 c 117 g 148 t
ORIGIN

Query Match 92.7%; Score 471; DB 9; Length 497;
Best Local Similarity 99.8%; Pred. No. 5.5e-116;
Matches 482; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

26 TGGATACCCGAGGCGCAACAGCGGCGGAGAGAGCGTTGACGTGAAAAAGT 85
1 TGGATACCCGAGGCGCAACAGCGGCGGAGAGAGCGTTGACGTGAAAAAGT 60
86 GGAATGACGAGCCCTCTGGGCTGGGATATTGGTGTGATTAAGTCCATCTGCAGA 145
61 GGAATGACGAGCCCTCTGGGCTGGGATATTGGTGTGATTAAGTCCATCTGCAGA 120
146 ACCACATTATGATCTTGGCATAGATGTCAAGCTAACAGGCGTCCGCTTTCAGAG 205
121 ACCACATTATGATCTTGGCATAGATGTCAAGCTAACAGGCGTCCGCTTTCAGAG 180
206 AGTACTGTGACGAGGAGCTGTACCACTGTTTCACTGACGACGACCTGCTTCTGCT 265
|||||

Db 181 AGTACTGTGACGAGGAGCTGTACCACTGTTTCACTGACGACCTGCTTCTGCT 240
Qy 266 GGCCTCAAAACACAGCAGGTGTGTCATTTGACACAGAGAGTGGAAATTC:AAAGATG 325
Db 241 GGCCTCAAAACACAGCAGGTGTGTCATTTGACACAGAGAGTGGAAATTC:AAAGATG 300
Qy 326 GGCACATGAGAAAGACATTTTCATCAAGCTTAATTTTGTATTATTCATTTTACT 385
Db 301 GGCACATGAGAAAGACATTTTCATCAAGCTTAATTTTGTATTATTCATTTTACT 359
Qy 386 TTCCCTGCTGTACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 445
Db 360 TTCCCTGCTGTACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 419
Qy 446 TCAGTTTCTGCTTCTGTAGCCATTTGATTTCTGTGTCAATTAATTAATTAATTAATTC 505
Db 420 TCAGTTTCTGCTTCTGTAGCCATTTGATTTCTGTGTCAATTAATTAATTAATTAATTC 479
Qy 506 TGG 508
Db 480 TGG 482
|||

RESULT 5
AX212267 3208 bp DNA linear PAT 06-SEP-2001
LOCUS
DEFINITION Sequence 27 from Patent WO0159134.
ACCESSION AX212267
VERSION AX212267.1 GI:15524031
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 3208)
Donoho, G., Scoville, J., Turner, C.A., Friedrich, G.B., Abuin, A., Zambrowicz, B. and Sands, A.T.
Human proteases and polynucleotides encoding the same
Patent: WO 0159134-A 27 16-AUG-2001;
Lexicon Genetics Incorporated (US)
JOURNAL
TITLE
AUTHORS
REFERENCES

FEATURES
source
Location/Qualifiers
1..3208
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 862 a 750 c 772 g 804 t
ORIGIN

Query Match 81.7%; Score 415; DB 6; Length 3208;
Best Local Similarity 98.6%; Pred. No. 6.9e-101;
Matches 429; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 74 AAGTGAAAAAGTGAATGACATGACCTCTGGGCTGGGATATTGTGATTAAGTGTG 133
Db 2765 AAAAAAAGTGAATGACATGACCTCTGGGCTGGGATATTGTGATTAAGTGTG 2824
Qy 134 CCATCTGAGACACACATTTATGATCTTTTCATAGAAATGTCAAGCTAACAGGCGTCCG 193
Db 2825 CCATCTGAGACACACATTTATGATCTTTTCATAGAAATGTCAAGCTAACAGGCGTCCG 2884
Qy 194 CTACTTCGAGAGAGTGTCTGCGATGGGAGAGTGTGAACATGCTTTTCACTTCCACT 253
Db 2885 CTACTTCGAGAGAGTGTCTGCGATGGGAGAGTGTGAACATGCTTTTCACTTCCACT 2944
Qy 254 GCATCTGCTGCTGCTCAAAACAGACAGTGTGTCAATTTGAGACAGAGAGTGGAAAT 313
Db 2945 GCATCTGCTGCTGCTCAAAACAGACAGTGTGTGTCAATTTGAGACAGAGAGTGGAAAT 3004
Qy 314 TCCAAAATATAGGAGCCTAGAGAAAGACTTTTCATATACCTTAATTTTGTATTC 373
Db 3005 TCCAAAATATAGGAGCCTAGAGAAAGACTTTTCATATACCTTAATTTTGTATTC 3064
Qy 374 ATTAAATGATTTTCCGCTGTTACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 433
|||||

Db 3065 ATTAA-TGACTTCCCTGCTGTACCTAATTACAAATTGATGAGACTGTCTTTTTC 3123

QY 434 TGCCTTTGTTTTCAGTTTGTCTGTCTAGCCATATGTTCTGTGTCACAAATTAAGT 493

Db 3124 TGCCTTTGTTTTCAGTTTGTCTGTCTAGCCATATGTTCTGTGTCACAAATTAAGT 3183

QY 494 CCAGTTGATTCCTG 508

Db 3184 CCAGTTGATTCCTG 3198

RESULT 6

LOCUS G27926 433 bp DNA linear STS 29-JUN-1996

DEFINITION human STS SHGC-34633, sequence tagged site.

ACCESSION G27926

VERSION G27926.1 GI:1396645

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 433)

AUTHORS Myers,R.M.

JOURNAL Unpublished (1996)

COMMENT

Contact: Richard M. Myers

Stanford Human Genome Center (SHGC)

Stanford University School of Medicine

Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 415/7259687

Fax: 415/7259689

Email: myerseshgc.stanford.edu

Primer A: CAGATCCAACTGACTTATTTG

Primer B: TATTCATTTAATGACTTCCCTGC

STS size: 139

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Tag Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from D52875

-- Washington University/Merck EST sequence.

Location/Qualifiers

FEATURES

source

1. .433

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="10"

STS

primer_bind

1. .24

primer_bind

complement(115..139)

BASE COUNT 139 a 100 c 87 g 107 t

ORIGIN

Query Match 77.2% Score 392; DB 11; Length 433;

Best Local Similarity 98.2%; Pred. No. 9.9e-95;

Matches 428; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY 72 TGAAGGAAAGTGAATGACAGTACCCCTGGGCGCTGGATATTTGGTGTGATACTG 131

Db 433 TGAAGGAAAGTGAATGACAGTACCCCTGGGCGCTGGATATTTGGTGTGATACTG 375

QY 132 TGCCATCTGACAGAACCCATTTATGATTTTGCATAGATGTCAAGCTAACAGGCTG 191

Db 374 TGCCATCTGACAGAACCCATTTATGATTTTGCATAGATGTCAAGCTAACAGGCTG 315

QY 192 CCCTACTTCAGAGAGTACTGTGCGATGGGAGTGTGTAACCATGCTTTTCACTTCA 251

Db 314 CCCTACTTCAGAGAGTACTGTGCGATGGGAGTGTGTAACCATGCTTTTCACTTCA 256

QY 252 CCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311

Db 255 CCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 196

QY 312 ATTCCAAAGTATGGGACATAGAGAAAGACTTCTCCATCAAGCTTAATTTGTAT 371

Db 195 ATTCCAAAGTATGGGACATAGAGAAAGACTTCTCCATCAAGCTTAATTTGTAT 136

QY 372 TCATTTAATGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431

Db 135 TCATTTAATGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 77

QY 432 TCGCTTTGTTTTCAGTTTGTCTGTCTGTAGCCATTTATTTCTGTGCAATAA 491

Db 76 TCGCTTTGTTTTCAGTTTGTCTGTCTGTAGCCATTTATTTCTGTGCAATAA 17

QY 492 GTCCAGTTGATTCG 507

Db 16 GTCCAGTTGATTCG 1

RESULT 7

LOCUS AC109638 104787 bp DNA linear PRI 09-MAR-2002

DEFINITION Homo sapiens BAC clone RP11-495B16 from 2, complete sequence.

ACCESSION AC109638 AC069095

VERSION AC109638.2 GI:18767595

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 104787)

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

PUBMED 9847074

REFERENCE

AUTHORS 2 (bases 1 to 104787)

TITLE Walligorski,J. and Cotton,M.

JOURNAL The sequence of Homo sapiens BAC clone RP11-495B16

UNPUBLISHED (2001)

REFERENCE

AUTHORS 3 (bases 1 to 104787)

TITLE Waterston,R.H.

JOURNAL Direct Submission

UNPUBLISHED (06-FEB-2002) Genome Sequencing Center, Washington

REFERENCE

AUTHORS 4 (bases 1 to 104787)

TITLE Waterston,R.H.

JOURNAL Direct Submission

UNPUBLISHED (20-FEB-2002) Genome Sequencing Center, Washington

UNIVERSITY SCHOOL OF MEDICINE, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE

AUTHORS 5 (bases 1 to 104787)

TITLE Waterston,R.

JOURNAL Direct Submission

UNPUBLISHED (09-MAR-2002) Department of Genetics, Washington

UNIVERSITY, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Feb 20, 2002 this sequence version replaced g1:16543153.

----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0495B16
 Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Pateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-563E24, 2000 bp overlap; the clone sequenced to the right is RP11-388N13. Actual start of this clone is at base position 13943 of RP11-563E24; actual end is at base position 104787 of RP11-495B16.

FEATURES

SOURCE

The sequence of AC069095 has been incorporated into AC109638.

Location/Qualifiers
 1..104787
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-495B16"
 /clone_lib="RPCT-11"
 552..596
 /rpt_family="AT_rich"
 repeat_region
 2637..3165
 /rpt_family="L2"
 repeat_region
 3182..3356
 /rpt_family="L2"
 repeat_region
 3818..3893
 /rpt_family="MER2_type"
 repeat_region
 4009..4191
 /rpt_family="MER2_type"
 repeat_region
 4666..5182
 /rpt_family="L2"
 repeat_region
 5799..5818
 /rpt_family="(A)n"
 repeat_region
 6192..6528
 /rpt_family="MER2_type"
 repeat_region
 6700..6769
 /rpt_family="MERL_type"

repeat_region 6786..6959
 /rpt_family="MERL_type"
 repeat_region 6973..7025
 /rpt_family="(TC)n"
 repeat_region 7025..7057
 /rpt_family="(CA)n"
 repeat_region 7319..7785
 /rpt_family="ERV1"
 repeat_region 9500..10052
 /rpt_family="ERV1"
 repeat_region 10697..10820
 /rpt_family="MALR"
 repeat_region 10821..11231
 /rpt_family="MALR"
 repeat_region 11232..11468
 /rpt_family="MALR"
 repeat_region 11703..11724
 /rpt_family="AT_rich"
 repeat_region 12494..12548
 /rpt_family="MER2_type"
 repeat_region 12549..12940
 /rpt_family="MALR"
 repeat_region 12941..13189
 /rpt_family="MER2_type"
 repeat_region 13185..13261
 /rpt_family="MER2_type"
 repeat_region 14239..14260
 /rpt_family="AT_rich"
 repeat_region 14475..15193
 /rpt_family="L1"
 repeat_region 15747..15887
 /rpt_family="L1"
 repeat_region 15967..15992
 /rpt_family="AT_rich"
 repeat_region 16107..16127
 /rpt_family="AT_rich"
 repeat_region 16180..16303
 /rpt_family="MERL_type"
 repeat_region 16304..16612
 /rpt_family="MERL_type"
 repeat_region 16653..16825
 /rpt_family="L1"
 repeat_region 16858..17337
 /rpt_family="L1"
 repeat_region 17354..18118
 /rpt_family="L1"
 repeat_region 18119..18142
 /rpt_family="(TTG)n"
 repeat_region 18143..18402
 /rpt_family="Alu"
 repeat_region 18403..18849
 /rpt_family="L1"
 repeat_region 18853..18956
 /rpt_family="L1"
 repeat_region 18957..19008
 /rpt_family="MALR"
 repeat_region 19011..19414
 /rpt_family="L1"
 repeat_region 19419..19458
 /rpt_family="CT_rich"
 repeat_region 19558..19858
 /rpt_family="Alu"
 repeat_region 19900..19920
 /rpt_family="AT_rich"
 repeat_region 19946..19973
 /rpt_family="AT_rich"
 repeat_region 21137..21158
 /rpt_family="AT_rich"
 repeat_region 21636..21721
 /rpt_family="CT_rich"
 repeat_region 23013..23036
 /rpt_family="AT_rich"
 repeat_region 24267..24310

